

1/11

## HPV 31 L1 nucleotide sequence alignment.

31 L1 wt	( 1)	ATGTCTCTGTGGCGGCCTAGCGAGGCTACTGTCTACTTACCACCTGTCCC
31 L1 partial	( 1)	.....
31 L1 total	( 1)	.....T.....A.A..ATCT..A.....C.....G.....A.....
31 L1 wt	( 51)	AGTGTCTAAAGTTGTAAGCACGGATGAATATGTAACACGAACCAACATAT
31 L1 partial	( 51)	.....
31 L1 total	( 51)	...C.....G..C..CTCT..C..C.....C..C..CA.....C.
31 L1 wt	( 101)	ATTATCACGCAGGCAGTGCTAGGCTGCTTACAGTAGGCCATCCATATTAT
31 L1 partial	( 101)	.....
31 L1 total	( 101)	.C..C.....T..TTC.....AT..T.G..C..C..T..C.....C..C
31 L1 wt	( 151)	TCCATACCTAAATCTGACAATCCTAAAAAATAGTTGTACCAAAGGTGTC
31 L1 partial	( 151)	.....
31 L1 total	( 151)	..T..C..A..G.....C..A..G..G..C..C..C.....C..
31 L1 wt	( 201)	AGGATTACAATATAGGGTATTTAGGGTTCGTTTACCAGATCCAAACAAAT
31 L1 partial	( 201)	.....
31 L1 total	( 201)	T..T..G.....C..A..C..C..A..CA.A..G.....C.....G.
31 L1 wt	( 251)	TTGGATTTCTGATACATCTTTTATAATCCTGAAACTCAACGCTTAGTT
31 L1 partial	( 251)	.....
31 L1 total	( 251)	.C..T..C..A..C..C.....C..C..C..A.....C...A.A..G..C
31 L1 wt	( 301)	TGGGCCTGTGTTGGTTTAGAGGTAGGTCGCGGGCAGCCATTAGGTGTAGG
31 L1 partial	( 301)	.....
31 L1 total	( 301)	.....T.....C.....G..A..C...A.A..T..A.....G.....C..
31 L1 wt	( 351)	TATTAGTGGTCATCCATTATTAAATAAATTTGATGACACTGAAAACCTCTA
31 L1 partial	( 351)	.....
31 L1 total	( 351)	...CTC.....C.....G..G..C..G..C..C.....C.....
31 L1 wt	( 401)	ATAGATATGCCGGTGGTCCTGGCACTGATAATAGGGAATGTATATCAATG
31 L1 partial	( 401)	.....
31 L1 total	( 401)	.C.....C..T.....A..T..C..C..C..A.....C..T...

FIG. 1A

2/11

31 L1 wt	( 451)	GATTATAAACAAACACAACACTGTGTTTACTTGGTTGCAAACCACCTATTGG
31 L1 partial	( 451)	.....
31 L1 total	( 451)	..C..C..G....C...T.....GT.G....T..G....A..C..
31 L1 wt	( 501)	AGAGCATTGGGGTAAAGGTAGTCCTTGTAGTAACAATGCTATTACCCCTG
31 L1 partial	( 501)	.....
31 L1 total	( 501)	T..A..C.....G...TC...A...TC.....C.....C.....A.
31 L1 wt	( 551)	GTGATTGTCCTCCATTAGAATTAAAAAATTCAGTTATACAAGATGGGGAT
31 L1 partial	( 551)	.....
31 L1 total	( 551)	....C.....A.....G.....G..G..C..T..C..C.....C..T..C
31 L1 wt	( 601)	ATGGTTGATACAGGCTTTGGAGCTATGGATTTTACTGCTTTACAAGACAC
31 L1 partial	( 601)	.....
31 L1 total	( 601)	.....C..C..C..T..C..T.....C..C..C.....G.....
31 L1 wt	( 651)	TAAAAGTAATGTTTCCTTTGGACATTTGTAATTCTATTTGTAAATATCCAG
31 L1 partial	( 651)	.....
31 L1 total	( 651)	C..GTC...C..C..A.....C.....C.....C.....G..C....
31 L1 wt	( 701)	ATTATCTTAAATGGTTGCTGAGCCATATGGCGATACATTATTTTTTTAT
31 L1 partial	( 701)	.....C.....C..C..G..C..C..C
31 L1 total	( 701)	.C..CT.G..G....C.....A.....C.....C..C..G..C..C..C
31 L1 wt	( 751)	TTACGTAGGGAACAAATGTTTGTAAAGGCATTTTTTTAATAGATCAGGCAC
31 L1 partial	( 751)	..G.....A.....G.....C.....C..C..C..C.....C.....
31 L1 total	( 751)	..G.....A.....G.....C.....C..C..C..C.....C.....
31 L1 wt	( 801)	GGTTGGTGAATCGGTCCCTACTGACTTATATATTAAAGGCTCCGGTTCAA
31 L1 partial	( 801)	C..A.....T.....A..C...C.G..C..C..G.....C.
31 L1 total	( 801)	C..A.....T.....A..C...C.G..C..C..G.....C.
31 L1 wt	( 851)	CAGCTACTTTAGCTAACAGTACATACTTTCCTACACCTAGCGGCTCCATG
31 L1 partial	( 851)	.C.....CC.G.....TCC..C.....C..A..T..ATCT.....
31 L1 total	( 851)	.C.....CC.G.....TCC..C.....C..A..T..ATCT.....
31 L1 wt	( 901)	GTTACTTCAGATGCACAAATTTTAAATAAACCATATTGGATGCAACGTGC
31 L1 partial	( 901)	..C..C..C..C..T..G..C..C..C..G.....C.....G.....
31 L1 total	( 901)	..C..C..C..C..T..G..C..C..C..G.....C.....G.....

FIG. 1B

3/11

31 L1 wt	( 951)	TCAGGGACACAATAATGGTATTTGTTGGGGCAATCAGTTATTTGTTACTG
31 L1 partial	( 951)	A.....T.....C..C.....C.....T..C...C.G..C..G....
31 L1 total	( 951)	A.....T.....C..C.....C.....T..C...C.G..C..G....
31 L1 wt	(1001)	TGGTAGATACCACACGTAGTACCAATATGTCTGTTTGTGCTGCAATTGCA
31 L1 partial	(1001)	....C.....G...TC.....C.....C.....C...T
31 L1 total	(1001)	....C.....G...TC.....C.....C.....C...T
31 L1 wt	(1051)	AACAGTGATACTACATTTAAAAGTAGTAATTTTAAAGAGTATTTAAGACA
31 L1 partial	(1051)	...TC...C.....C..C..GTCCTC...C..C..G.....CC.G.....
31 L1 total	(1051)	...TC...C.....C..C..GTCCTC...C..C..G.....CC.G.....
31 L1 wt	(1101)	TGGTGAGGAATTTGATTTACAATTTATATTTTCAGTTATGCAAAATAACAT
31 L1 partial	(1101)	.....C...C.G.....C..C..C.....G.....G..C..CC
31 L1 total	(1101)	.....C...C.G.....C..C..C.....G.....G..C..CC
31 L1 wt	(1151)	TATCTGCAGACATAATGACATATATTCACAGTATGAATCCTGCTATTTTG
31 L1 partial	(1151)	.G.....T.....C.....C..C..C.....C.....C..CC..
31 L1 total	(1151)	.G.....T.....C.....C..C..C.....C.....C..CC..
31 L1 wt	(1201)	GAAGATTGGAATTTTGGATTGACCACACCTCCCTCAGGTTCTTTGGAGGA
31 L1 partial	(1201)	..G..C.....C..C..TC.....T..A..T..C.....
31 L1 total	(1201)	..G..C.....C..C..TC.....T..A..T..C.....A..
31 L1 wt	(1251)	TACCTATAGGTTTGTAACTCACAGGCCATTACATGTCAAAAAGTGCCC
31 L1 partial	(1251)	.....
31 L1 total	(1251)	C.....C..A..C..C.....T..A..T..C..C.....GTC...T.
31 L1 wt	(1301)	CCCAAAAGCCCAAGGAAGATCCATTTAAAGATTATGTATTTTGGGAGGTT
31 L1 partial	(1301)	.....
31 L1 total	(1301)	.A.....A.....C.....C..G..C..C..C.....A..C
31 L1 wt	(1351)	AATTTAAAAGAAAAGTTTTCTGCAGATTTAGATCAGTTTCCACTGGGTCG
31 L1 partial	(1351)	.....
31 L1 total	(1351)	..C..G..G.....C.....T..C..G..C..A..C...T....A.
31 L1 wt	(1401)	CAAATTTTATTACAGGCAGGATATAGGGCACGTCTAAATTTAAAGCAG
31 L1 partial	(1401)	.....
31 L1 total	(1401)	A..G..C..G..G..A..T..T..C..A..TA..A..A..G..C..G..T.

FIG.1C

4/11

31 L1 wt	(1451)	GTAAACGTAGTGCACCCTCAGCATCTACCACTACACCAGCAAAACGTAAA
31 L1 partial	(1451)	.....
31 L1 total	(1451)	....GA.ATC...T..A..T..T.....C..C.....T..GA.A..G
31 L1 wt	(1501)	AAAACTAAAAAGTAA (SEQ ID NO:1)
31 L1 partial	(1501)	..... (SEQ ID NO:2)
31 L1 total	(1501)	..... (SEQ ID NO:3)

FIG.1D

5/11

HPV31 L1 total rebuild nucleotide and amino acid sequences.

M S L W R P S E A T V Y L P P V P  
1 ATGTCTTTGT GGAGACCATC TGAAGCTACC GTCTACTTGC CACCAGTCCC

V S K V V S T D E Y V T R T N I Y  
51 AGTCTCTAAG GTCGTCTCTA CCGACGAATA CGTCACCAGA ACCAACATCT

Y H A G S A R L L T V G H P Y Y  
101 ACTACCACGC TGGTTCTGCT AGATTGTTGA CCGTCGGTCA CCCATACTAC

S I P K S D N P K K I V V P K V S  
151 TCTATCCCAA AGTCTGACAA CCCAAAGAAG ATCGTCGTCC CAAAGGTCTC

G L Q Y R V F R V R L P D P N K F  
201 TGGTTTGCAA TACAGAGTCT TCAGAGTCAG ATTGCCAGAC CCAAACAAGT

G F P D T S F Y N P E T Q R L V  
251 TCGGTTTCCC AGACACCTCT TTCTACAACC CAGAAACCCA AAGATTGGTC

W A C V G L E V G R G Q P L G V G  
301 TGGGCTTGTG TCGGTTTGGA AGTCGGTAGA GGTCAACCAT TGGGTGTCGG

I S G H P L L N K F D D T E N S N  
351 TATCTCTGGT CACCCATTGT TGAACAAGTT CGACGACACC GAAAACCTCTA

R Y A G G P G T D N R E C I S M  
401 ACAGATACGC TGGTGGTCCA GGTACCGACA ACAGAGAATG TATCTCTATG

D Y K Q T Q L C L L G C K P P I G  
451 GACTACAAGC AAACCCAATT GTGTTTGTTG GGTGTGAAGC CACCAATCGG

E H W G K G S P C S N N A I T P G  
501 TGAACACTGG GGTAAGGGTT CTCCATGTTC TAACAACGCT ATCACCCCAG

D C P P L E L K N S V I Q D G D  
551 GTGACTGTCC ACCATTGGAA TTGAAGAACT CTGTCATCCA AGACGGTGAC

FIG. 2A

6/11

M V D T G F G A M D F T A L Q D T  
601 ATGGTCGACA CCGGTTTCGG TGCTATGGAC TTCACCGCTT TGCAAGACAC

K S N V P L D I C N S I C K Y P D  
651 CAAGTCTAAC GTCCATTGG ACATCTGTAA CTCTATCTGT AAGTACCCAG

Y L K M V A E P Y G D T L F F Y  
701 ACTACTTGAA GATGGTCGCT GAACCATACG GCGACACCTT GTTCTTCTAC

L R R E Q M F V R H F F N R S G T  
751 TTGCGTAGAG AACAGATGTT CGTAAGGCAC TTCTTCAACA GATCCGGCAC

V G E S V P T D L Y I K G S G S T  
801 CGTAGGTGAA TCTGTCCCAA CCGACCTGTA CATCAAGGGC TCCGGTTCCA

A T L A N S T Y F P T P S G S M  
851 CCGCTACCCT GGCTAACTCC ACCTACTTCC CAACTCCATC TGGCTCCATG

V T S D A Q I F N K P Y W M Q R A  
901 GTCACCTCCG ACGCTCAGAT CTTCAACAAG CCATACTGGA TGCAGCGTGC

Q G H N N G I C W G N Q L F V T V  
951 ACAGGGTCAC AACAACGGTA TCTGTTGGGG TAACCAGCTG TTCGTGACTG

V D T T R S T N M S V C A A I A  
1001 TGGTCGATAC CACGCGTTCT ACCAACATGT CTGTCTGTGC TGCAATCGCT

N S D T T F K S S N F K E Y L R H  
1051 AACTCTGACA CTACCTTCAA GTCCTCTAAC TTCAAGGAGT ACCTGAGACA

G E E F D L Q F I F Q L C K I T L  
1101 TGGTGAGGAA TTCGATCTGC AATTCATCTT CCAGTTGTGC AAGATCACCC

S A D I M T Y I H S M N P A I L  
1151 TGTCTGCTGA CATCATGACC TACATCCACA GTATGAACCC TGCCATCCTG

E D W N F G L T T P P S G S L E D  
1201 GAGGACTGGA ACTTCGGTCT GACCACTCCA CCTTCCGGTT CTTTGGAAGA

FIG.2B

7/11

T Y R F V T S Q A I T C Q K S A P  
1251 CACCTACAGA TTCGTCACCT CTCAAGCTAT CACCTGTCAA AAGTCTGCTC

Q K P K E D P F K D Y V F W E V  
1301 CACAAAAGCC AAAGGAAGAC CCATTCAAGG ACTACGTCTT CTGGGAAGTC

N L K E K F S A D L D Q F P L G R  
1351 AACTTGAAGG AAAAGTTCTC TGCTGACTTG GACCAATTCC CATTGGGTTAG

K F L L Q A G Y R A R P K F K A G  
1401 AAAGTTCTTG TTGCAAGCTG GTTACAGAGC TAGACCAAAG TTCAAGGCTG

K R S A P S A S T T T P A K R K  
1451 GTAAGAGATC TGCTCCATCT GCTTCTACCA CCACCCCAGC TAAGAGAAAAG

K T K K \* (SEQ ID NO:4)  
1501 AAGACCAAGA AGTAA (SEQ ID NO:3)

FIG.2C

SUMMARY OF HPV 31 SEQUENCES.

L1 CONSTRUCT	NUCLEOTIDES	AMINO ACIDS	NUCLEOTIDE IDENTITY	AMINO ACID IDENTITY	COMMENTS
HPV 31 LA WILD-TYPE	1515	504			
HPV 31 L1 PARTIAL REBUILD	1515	504	92%	100%	121 CHANGES BETWEEN nt 697-1249
HPV 31 L1 TOTAL REBUILD	1515	504	75%	100%	376 CHANGES BETWEEN nt 1-1515

FIG.3



9/11

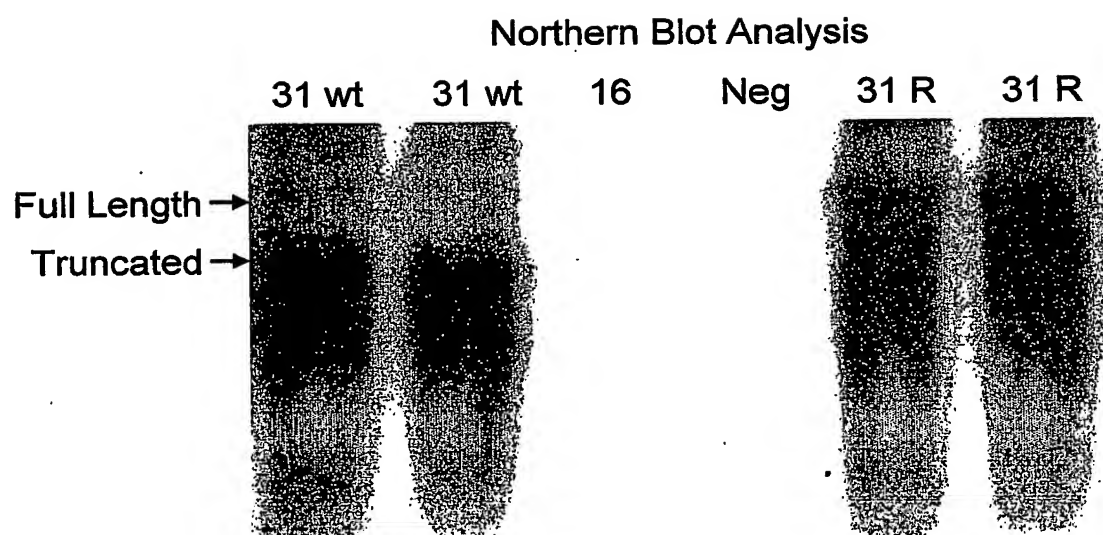


FIG.4

10/11

## RESULTS FROM RADIOIMMUNOASSAY

EXP.	L1 CONSTRUCT	PROTEIN CONCENTRATION (mg/ml)	RIA MINUS BACKGROUND (cpm/ml)	31 L1 VLP*/ mg protein (cpm/mg)	AVERAGE (cpm/mg)	RATIO (Ave/Ave)
1	31 WILD-TYPE	1.64	414	252	460	1 (31 wt/31 wt)
		1.62	987	609		
		1.82	904	497		
		1.76	844	480		
1	31 PARTIAL REBUILD	1.67	5061	3031	3158	6.9 (31 PARTIAL/31 wt)
		1.55	5091	3285		
2	31 PARTIAL REBUILD	2.27	3901	1719	2095	1 (31 PARTIAL/31 PARTIAL)
		2.27	4081	1798		
		2.38	7135	2998		
		2.38	4428	1861		
2	31 TOTAL REBUILD	2.07	6628	3202	3645	1 (31 TOTAL/31 PARTIAL)
		2.07	8461	4087		

FIG. 5

11/11

Transmission Electron Microscopy

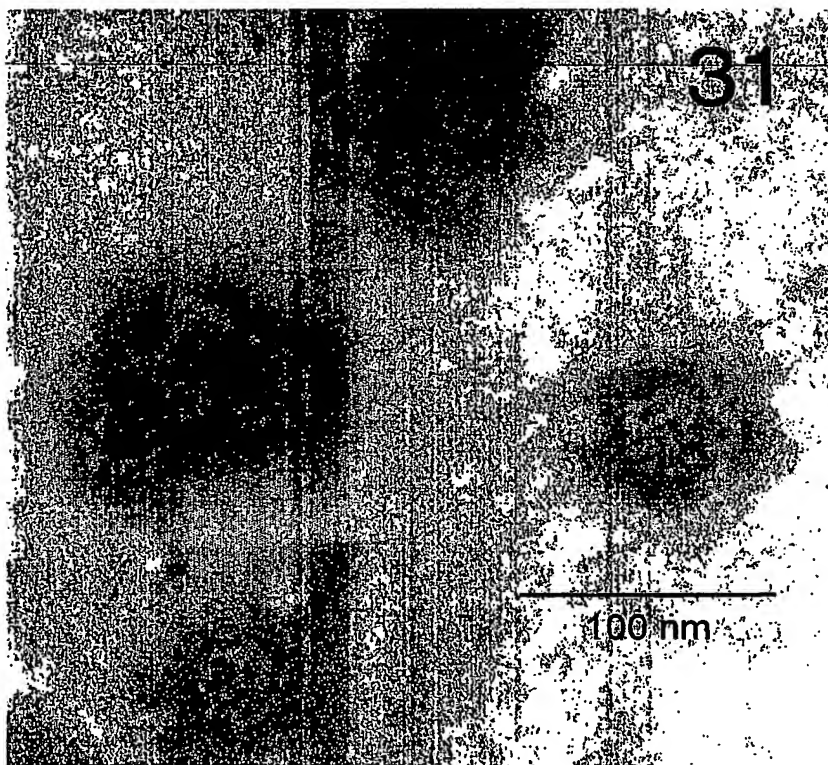


FIG.6